

(FILE 'HOME' ENTERED AT 14:18:51 ON 29 NOV 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 14:18:55 ON 29 NOV
2004

L1 88921 S ZEA (2N) MAYS
L2 25 S L1 AND EXONUCLEASE
L3 17 DUP REM L2 (8 DUPLICATES REMOVED)

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	2284	79.7	705	2	Q7XQR9	Q7xqr9 oryza sativ
2	2020.5	70.5	720	1	MR11_ARATH	Q9xgm2 arabidopsis
3	1571.5	54.9	615	2	Q6ZBS2	Q6zbs2 oryza sativ
4	1571.5	54.9	615	2	BAD03045	Bad03045 oryza sat
5	1571.5	54.9	615	2	BAD03241	Bad03241 oryza sat
6	958.5	33.5	708	1	MR11_HUMAN	P49959 homo sapien
7	958.5	33.5	708	2	AAH63458	Aah63458 homo sapi
8	958.5	33.5	708	2	AAS79320	Aas79320 homo sapi
9	949	33.1	706	1	MR11_MOUSE	Q61216 mus musculu
10	948.5	33.1	711	1	MR11_XENLA	Q9w6k1 xenopus lae
11	946	33.0	513	2	Q8BRV3	Q8brv3 mus musculu
12	940	32.8	706	1	MR11_RAT	Q9jim0 rattus norv
13	929.5	32.5	619	2	Q7T397	Q7t397 brachydanio
14	919.5	32.1	731	1	MR11_COPCI	Q9uvn9 coprinus ci
15	907.5	31.7	700	1	MR11_CHICK	Q9iam7 gallus gall

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	2020.5	70.5	720	2	T52564	Mre11 protein homo
2	852.5	29.8	649	1	S58097	probable dna repai
3	768	26.8	692	1	S57592	probable phospho
4	724	25.3	772	2	T27512	hypothetical prote
5	178	6.2	443	1	G69378	probable phospho
6	175.5	6.1	423	2	E75103	phosphoesterase ho
7	174.5	6.1	413	1	D71083	probable phospho
8	163.5	5.7	587	1	E69171	phosphoesterase-re
9	150.5	5.3	381	2	C90395	DNA repair protein
10	143	5.0	1038	2	JC5497	claustrin - chick

RESULT 4
US-10-425-115-230925
; Sequence 230925, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 230925
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(726)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_142196C.1.pep
US-10-425-115-230925

Query Match 88.7%; Score 2539; DB 17; Length 726;
Best Local Similarity 90.6%; Pred. No. 1.3e-199;
Matches 499; Conservative 0; Mismatches 0; Indels 52; Gaps 2;

Qy	25	MSEPAQPSGGEGDVNTLRILVATDCHLGYMEKDEIRRFDSFQAFEEICALADKNKVDFIL	84
Db	1	MSEPAQPSGGEGDVNTLRILVATDCHLGYMEKDEIRRFDSFQAFEEICALADKNKVDFIL	60
Qy	85	LGGDLFHENKPSRSTLVKTIEILRRYCLNDQPVKFQVVSQTVNFPNRFGKVNYEDPNFN	144
Db	61	LGGDLFHENKPSRSTLVKTIEILRRYCLNDQPVKFQVVSQTVNFPNRFGKVNYEDPNFN	120
Qy	145	VGLPVFTIHGNHDDPAGVDNLSAIDILSACNLVNYFGKMDLGGSGVGQIAVYPVLVKGM	204
Db	121	VGLPVFTIHGNHDDPAGVDNLSAIDILSACNLVNYFGKMDLGGSGVGQIAVYPVLVKGM	180
Qy	205	TSVALYGLGNIRDERLNRMFQTPHSVQWMRPGTQDGESASDWFNILVLHQNRKTNPKSA	264
Db	181	TSVALYGLGNIRDERLNRMFQTPHSVQWMRPGTQDGESASDWFNILVLHQNRKTNPKSA	240
Qy	265	INEHFL-----PGSSVATSLIDGEAKPKHVLLLE	293
Db	241	INEHFLPRFLDFIVWGHEHECLIDPQEVPGMGFHTQPGSSVATSLIDGEAKPKHVLLLE	300
Qy	294	IKGNQYRPTKIPRLSVPFNEYAEVVLKDEADVNSNDQDSVLEHLDKIVRNLIIEKSSQPTA	353
Db	301	IKGNQYRPTKIPRLSVPFNEYAEVVLKDEADVNSNDQDSVLEHLDKIVRNLIIEKSSQPTA	360
Qy	354	SRSEPKLPLVRIKVDSGFSTINPQRFGQKYVGKVANPQDILIFSKSAKKRQTTGDHIDD	413

Db	361	SRSEPKLPLVRIKV DYS GFSTINPQR FGQKYVGKVANPQDILIFS KSAKKRQTTGDHIDD	420
Qy	414	SEKLRPEELNQQTIEALVAESNL-----KMEILPVDDLDIALHD	452
Db	421	SEKLRPEELNQQTIEALVAESNLXFTAHYLDMRMMFCEDHFIFXKMEILPVDDLDIALHD	480
Qy	453	FVNKDDKMAFY SCLQRNLEETRNKLSSEADSKFEEEDIIVKVGECMQERVKERSLHSKD	512
Db	481	FVNKDDKMAFY SCLQRNLEETRNKLSSEADSKFEEEDIIVKVGECMQERVKERSLHSKD	540
Qy	513	GTRLTTGSHNL 523	
Db	541	GTRLTTGSHNL 551	

Database : Published_Applications_AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	2864	100.0	552	9	US-09-835-654-2	Sequence 2, Appli
2	2864	100.0	552	15	US-10-650-108-2	Sequence 2, Appli
3	2864	100.0	552	16	US-10-650-109-2	Sequence 2, Appli
4	2539	88.7	726	17	US-10-425-115-230925	Sequence 230925,
5	2201.5	76.9	490	15	US-10-425-114-53913	Sequence 53913, A
6	2200.5	76.8	497	15	US-10-425-114-64871	Sequence 64871, A
7	2135.5	74.6	554	16	US-10-437-963-184295	Sequence 184295,
8	2020.5	70.5	720	13	US-10-047-412A-8	Sequence 8, Appli
9	1571.5	54.9	615	16	US-10-437-963-204901	Sequence 204901,
10	958.5	33.5	708	13	US-10-087-192-1224	Sequence 1224, Ap
11	950	33.2	752	13	US-10-087-192-1221	Sequence 1221, Ap

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB	ID
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1	2864	100.0	552	4	US-09-835-654-2
2	2020.5	70.5	720	3	US-09-480-921B-8
3	954.5	33.3	680	4	US-09-538-092-1165
4	768	26.8	692	4	US-09-538-092-632
5	507.5	17.7	270	4	US-09-248-796A-19151
6	141.5	4.9	132	4	US-09-270-767-33195
7	141.5	4.9	132	4	US-09-270-767-48412
8	136	4.7	857	4	US-09-248-796A-20522
9	122	4.3	1120	3	US-09-147-404-1
10	122	4.3	1935	4	US-09-538-092-916
11	121	4.2	398	4	US-09-710-279-44
12	121	4.2	398	4	US-09-710-279-1498
13	121	4.2	417	3	US-09-134-001C-3810

RESULT 2

US-09-480-921B-8

; Sequence 8, Application US/09480921B
; Patent No. 6387637
; GENERAL INFORMATION:
; APPLICANT: Levin, Joshua Z.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Potter, Sharon L.
; APPLICANT: Wegrich, Lynette M.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30780A
; CURRENT APPLICATION NUMBER: US/09/480,921B
; CURRENT FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-09-480-921B-8

Query Match 70.5%; Score 2020.5; DB 3; Length 720;
Best Local Similarity 74.2%; Pred. No. 1.5e-189;
Matches 385; Conservative 62; Mismatches 37; Indels 35; Gaps 4;

Qy 39 NTLRILVATDCHLGYMEKDEIRRFDQAFEEICALADKNKVDIFILLGGDLFHENKPSRS 98
Db 8 DTLRVLVATDCHLGYMEKDEIRRHDQAFEEICSAECKQVDFLLLGGDLFHENKPSRT 67

Qy 99 TLVKTIEILRRYCLNDQPVKFQVVSQTVNFPNRFGVNVYEDPNFNVGLPVFTIHGNHDD 158
Db 68 TLVKAIEILRRHCLNDKPVQFQVVSQTVNFQNAFGQVNVYEDPHFNVGLPVFSIHGNHDD 127

Qy 159 PAGVDNLSAIDILSACNLVNYFGKMDLGGSGVGQIAVYPVLVKKGMTSVALYGLGNIRDE 218
Db 128 PAGVDNLSAIDILSACNLVNYFGKMLGGSGVGQITLYPILMKKGTTVALYGLGNIRDE 187

Qy 219 RLNRMFQTPHSVQWMRPGTQDGESASDWFNILVLHQNRKTNPKSAINEHFL----- 270
Db 188 RLNRMFQTPHAVQWMRPEVQEGCDVSDWFNILVLHQNRVKSNPNAISEHFLPRFLDFIV 247

Qy 271 -----PGSSVATSLIDGEAKPKHVLLIEIKGNQYRPTKIPRL 307
Db 248 WGHEHECLIDPQEVSQMGFHTQPGSSVATSLIDGESKPKHVLLIEIKGNQYRPTKIPLT 307

Qy 308 SVRPFEYAEVVLKDEADVNSNDQDSVLEHLDKIVRNLIIEKSSQPTASRSEPKLPLVRIKV 367
Db 308 SVRPFEYTEIVLKDESIDPNDQNSILEHLDKVVRLNIEKASKKAVNRSEIKLPLVRIKV 367

Qy 368 DYSGFSTINPQRFQKYVGKVANPQDILIFSKSAKKRQTTGDHIDDSEKLRPEELNQQTI 427
Db 368 DYSGFMTINPQRFQKYVGKVANPQDILIFSKASKKGRSEA-NIDDSERLRPEELNQQNI 426

Qy 428 EALVAESNLKMEILPVDDLDIALHDFVNKDDKMAFYSCQRNLEETRNKLSSEADSKFE 487
Db 427 EALVAESNLKMEILPVNDLDVALHNFVNKDDKLAFYSCVQYNLQETRGKLAQDAKKFE 486

Qy 488 EEDIIVKGECMQERVKERSLHSKDGR-LTTG--SHNL 523
|:|:|:|||||:|:|:|||:|||:|||:|||:|||:|||:|||:|||
Db 487 EDDLILKGECLEERLKDRSTRPTGSSQFLSTGLTSENL 525

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	3616	100.0	3616	6	AX460870 Sequence
2	3529.8	97.6	3665	9	BC013153 Homo sapi
3	3505.4	96.9	3607	6	BD175095 Nucleic a
4	2844.4	78.7	2976	6	AX323479 Sequence
5	2665.6	73.7	2736	9	AY036093 Homo sapi
6	2597.2	71.8	2603	6	AX377787 Sequence
7	2567.6	71.0	2592	6	AX817285 Sequence
8	2461.4	68.1	2599	6	AX817283 Sequence
9	2443.6	67.6	3608	4	AF529202 Bos tauru
10	2309	63.9	2402	6	AX780632 Sequence
11	2269.4	62.8	2271	9	AF338441 Homo sapi
12	2265.4	62.6	2322	9	BC007522 Homo sapi
13	2263.2	62.6	2268	6	AX323481 Sequence
14	2258.2	62.5	2271	9	AF395336 Homo sapi
15	2019.6	55.9	2059	9	AK025542 Homo sapi
16	1918.8	53.1	3767	6	BD269865 The poly
17	1730	47.8	2274	6	BD175096 Nucleic a
18	1730	47.8	2274	10	AF338440 Mus muscu